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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model	
Run on: August 7, 2003, 05:36:29; Search t (without 7315.604	time 1275 Seconds alignments; Willion cell updates/sec
Title: US-10-054-399A-1 Perfect score: 228 Sequence: 1 ccctctgtatacttttcaaaaa	aaacgctaatgaattccagc 228
Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
Searched: 2888711 seqs, 20454813386 residues	
Total number of hits satisfying chosen parameters:	5777422
Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database : GenEmbl:* 2	
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

c	AXO04383 Sequence BD078523 Yeast Cdc E61227 Nucleotide AXO04385 Sequence AXO04385 Sequence AXO04385 Sequence BD078525 Yeast Cdc BD078525 Yeast Cdc BD078525 Yeast Cdc BD078526 Yeast Cdc E61228 Nucleotide E61228 Nucleotide E61228 Nucleotide E61228 Nucleotide E61230 Nucleotide AX594660 Sequence AX594660 Sequence AX20812 Candida a AX488842 Sequence AX488842 Sequence AX488842 Sequence AX488842 Sequence AX488842 Sequence AX488842 Sequence U12538 S.pombe Chr AC025749 Genomic S AC017681 Oryza sat U32577 Rattus nor GG6443 human STS W AL713781 Homo sapien L32611 Homo sapien AC138470 Homo sapien AC138474 Homo sapien AC138532 Human DNA AC011274 Homo sapien AC138532 Human STS AC011274 Homo sapien AC138532 Human STS AC013875 Rattus no	linear PAT 24-AUG-2000
SUMMARIES ID		228 bp DNA 60 60 7. 1. 12,R.A. 115-APR-1999;
ery tch Length DB	0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0	13 1 from Pat 13 1 GI:9927 11c construct 11c construct 11cl sequence 11al sequence 11a
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BD078523.1 GI:22624126
BD078523.1 GI:22624126
Synthetic construct
Synthetic construct
artificial sequences.

E 1 (base1 to 228)
S Arkowitz,R.A. and Nern,P.M.A.
Yeast Cdc4pp variant lacking G protein beta-subunit bond
L Patent: UP 2001519158.A 1 23.0CT-2001;
HEDICAL RESEARCH COUNCIL
OS Artificial Sequence
PN JR 2001519158.A/1
PD 23.0CT-2091
PP 08-0CT-1998 JP 2005515009
MEDICAL RES COUNCIL (GB); NERN PETER MICHAEL ALJOSCHA (GB)
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/mol_type*genonic DNA*
/db_xref*taxon.32530*
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                                                                          /organism="synthetic construct"
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/db_xref="taxon:32644"
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BD078524 228 bp DNA linear PAT 27-AUG-2002 Yeast Cdc24p variant lacking G protein beta-subunit bond. BD078524
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/db_xref="taxon:32630"
/nofe="nucleic acid"
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                       Sequence 3 from Patent W09918213.
AX004385
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/organism="synthetic cor
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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61 GACGATTIGAAAGTCTGTAAAAAATCCATTTATGACTTTATATATTGGGCTGCAAGAAACAC 120
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Synthetic construct

synthetic construct

artificial sequences.

I (bases 1 to 228)

Arkowitz,R.A. and Nern,P.M.A.

Yeast cdc24p variant lacking G protein beta-subunit bond

Patent: JP 2001519188-A 4 23-OCT-2001;

MEDICAL RESEARCH COUNCIL

OS Artificial Sequence
PD 23-OCT-2001

PF 08-OCT-1998 JP 2000515009

PF 08-OCT-1998 JP 2000515009

PF 08-OCT-1998 JP 2000515009

PF 08-OCT-1998 JP 2000515009

PF 08-OCT-1997 GB 9721357.3,08-OCT-1997 GB 9721358.1 PR

12-UNU-1998 GB 9721357.3,08-OCT-1997 GB 9721358.1 PR

PI NROBERT ALAN ARKOWITZ, PETER MICHAEL ALJOSCHA NERN PC

C12N15/09,A61K88/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/
                                                   Description of Artificial Sequence: nucleic acid FH Location/Qualifiers
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Yeast Cd024p variant lacking G protein beta-subunit bond BD078526
BD078526.1 GI:22624129
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/organism-synthetic construct
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PN JP 2001519188-A/2
PN J9 CCT-2001519188-A/2
PF 08-OCT-1998 JP 2000515009
PR 08-OCT-1997 GB 9721357.3,08-OCT-1997 GB 9721358.1 PR
12-JUN-1998 GB 9812793.9
PT ROBERT ALAN ARKOWITZ, PETER MICHAEL ALJOSCHA NERN PC
C12N15/09,A61K39/00,A61K45/00,A61P43/00,CG7K14/82,C12Q1/68, PC
C12N15/00,A61K37/02
CC DESCRIPTION OF AFIRFICIAL SEQUENCE: nucleic acid FH Key
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                  artificial sequences.

I (bases 1 to 228)
Arkowitz,R.A. and Nern,P.M.A.
Yeast Cd24p variant lacking G protein beta-subunit bond
Patent: JP 2001519158-A 2 23-0CT-2001;
MEDICAL RESEARCH COUNCIL
OS Artificial Sequence
PN JP 2001519158-A/2
PD 31-0CT-2001
PF 08-0CT-1997 GB 9721357.3,08-0CT-1997 GB 9721358.1
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12-JUN-1998 GB 9812793.9
PI ROBERT ALAN ARKOWITZ, PETER MICHAEL ALJOSCHA NERN PC
C12N15/09,A61K38/00,A61K45/00,A61F43/00,C07K14/82,C12Q1/68,
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Patent: JP 2001519158-A 3 23-OCT-2001;
MEDICAL RESEARCH COUNCIL
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1. .28
//organism-"synthetic construct"
//mol_type-"genomic DNA"
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PR 08-OCT-1997 GB 9721357.
12-JUN-1998 GB 9812793.9
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artificial sequences.
1 (bases 1 to 228)
Arkowitz,R.A. and Nern,P.M.A.
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Patent: JP 199913578-A 3 27-APR-1999;
MEDICAL RESEARCH COUNCIL
OS Unidentified
DN JP 1999113578-A/3
PD 27-APR-1999
PF 21-OCT-1997 JP 1997326899
PR 08-OCT-1997 GB 97213581
PR ROBERT ALAN AROVITSU.PATER MICHAEL ARUYOSHA NERUN PC
C12N15/09,A61K31/70,A61K38/00,C07K14/395//C07K14/82,G01N33/15,
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                        228
  linear
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                                                                                                                                          linear

    .228
    /organism='Unidentified'.

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E62130. GI:13027200
JP 1999113578-A/4. unidentified
                                                                                                                                        E61229 228 bp UNA
Nucleotide sequence and protein sequence.
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/organism-"unidentified"
/mol_type-"genomic DNA"
/db_xref-"taxon:32644"
a 49 c 43 g 69
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Robert, A.A. and Pater, M.A.N.
                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 228)
Robert, A.A. and Pater, M.A.N.
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UP 1999113578-A/3.
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                                                                                                                                                                                                                                                                                                      unclassified.
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C12N15/09,
C12N15/00,
PC A61K3
PC TOPO1
FH KeY
FT SOURC
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L(bases 1 to 228)

AUTHORS

ROBERT.A.A. and Pater.M.A.N.

I (bases 1 to 228)

AUTHORS

ROBERT.A.A. and Pater.M.A.N.

INClectide sequence and protein sequence

JOURNAL Patent: JP 1999113578-A 2 27-APR-1999;

MEDICAL RESEARCH COUNCIL

MEDICAL RESEARCH COUNCIL

OS Unidentified

PD 27-APR-1999

PP 31-1999113578-A/2

PP 37-1997 GB

PP 08-OCT-1997 GB
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Pred. No. 2.3e-52;
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                        0; Mismatches
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/organism-"unidentified"
/orl_type="genomic DNA"
/db_txref="taxon:32644"
a 48 c 42 g 70
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COMMENT

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/protesin_id="Aaa82871.1"
/db_xref="G1:1100997"
/translation="MAIQTRRASGISISDLKPKPSATSISIPMONVMKPVTEQDSLF
/translation="MAIQTRRASGISISDLKPKPSATSISIPMONVMKPVTEQDSLF
/translation="MAIQTRRASGISISDLKPKPSATSISIPMONTLIFSMOHEDSSD
LAPTIRESSISTATIAMSMEGISYTNSMPSATPMMEDTLITFSMGILFTTMDCDPVTO
LSQLFQQGAPLCILFNSVKPQFKLPVIASDDLKVCKKSIYDFILGCKKHFAFNDEELF
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PREVKIKTEVEPSKTOKOLIMSPETLIMSSPTIFPSKSKTOQIMNAEDQHRHDPQOSSKKH
PREVKIKTEVEPSKORIGALEMHSKHFFKLYEPWSLGQNAALTEFLSSTLAKKRYDES
ORFIINNKLELOSFLYKPVORLCRYPLLVKELLAESSDDNYTKELEAALDISKNIARS
YLERISHOVYKKLSKORVWKKOYRISKYGELLYPDKYFTSTINSSSPEREFEV
YLERIIILESEVYRKKSASSLLILKKKSSTSASISASITDNNGSPHRSYHKSNSS
SSNNIHLSSSSAAAIIHSSTNSSDNNSNNSSSSLFKLSANFDKLDLKGRIMIMNLNO
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STYTSSTAKSSKMSPTTHNTPNHHRNRONDDAMSFESHEKRKVSVLPKRRTYS
SFESEIKSIESENFKASIPESSILFRISYNNNSNNTSSESIFTLLVEKVWFDDLIMAI
NSKISNTHNNISPITKIKYQDEDGDFVVLGSDEDWNVAKEMLAENNEKFLNIRLY
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Original source text: Yeast (S.cerevisiae strain YOC138-10A)) DNA,
clone pYOM105.
                                                                                                                                                                                                                                                                                                                                                                    YSCCLS4A 2811 bp DNA linear PLN 04-DBC-19
Yeast (S.cerevisiae) CLS4 gene encoding a Ca regulatory protein,
complete cds.
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1 (bases 1 to 2811)

Miyamoto.S., Ohya,Y. Sano,Y., Sakaguchi,S., Iida,H. and Anraku, Important for Ca(2+) modulated bud assembly
Biochem. Biophys. Res. Commun. 181 (2), 604-610 (1991)
                                        2 (bases 1 to 2811)
Miyamoto,S., Ohya,Y., Ohsumi,Y. and Anraku,Y.
Nucleotide sequence of the CLS4 (CDC24) gene of Saccharomyces
                                                                                                                                                                                                                                       /organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/db_xref="taxon:4932"
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/note="calcium regulatory protein"
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caclcium regulatory protein.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
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Eukaryota; Funqi: Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROBERT ALAN AKOVITTSU, PATER MICHAEL, ARUYOSHA NERUN PC
5/09, A61K31/70, A61K38/00, C07K14/395//C07K14/82, G01N33/15,
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/mol_type="genomic DNA"
/db_xref="taxon:4932"
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Pred. No. 6.6e-52;
0; Mismatches 2;
Nucleotide sequence and protein sequence
Patent: JP 1999113578-A 4 27-APR-1999;
MEDICAL RESEARCH COUNCIL
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Cloning and disruption of a gene required for growth on acetate but not on ethanol: the acetyl-coenzyme A synthetase gene of Saccharomyces cerevisiae
Yeast 8 (12), 1043-1081 (1992)
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Oliver, S.G., van der Aart, Q.J., Agostoni-Carbone, M.L., Aigle, M.,
Alberghina, L., Alexandraki, D., Antoine, G., Anwar, R., Ballesta, J.P.,
Benit, P. - The complete DNA sequence of yeast chromosome III
Nature, 357 (6373), 38-46 (1992)
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(by Virgilio, C., Burckert, N., Neuhaus, J.M., Boller, T. and Wiemkon, A. CNEI, a Saccharomyces cerevisiae homologue of the genes encoding mammalian calnexin and calreticulin

(sest 9 (2), 185-188 (1993)
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De Virgilio,C., Burckert,N., Barth,G., Neuhaus,J.M., Boller,T. and
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Proc. Natl. Acad. Sci. U.S.A. 89 (10), 4338-4342 (1992)
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Teunissen,A.W., Holub,E., van der Hucht,J., van den Berg,J.A. and
Nash,R., Tokiwa,G., Anand,S., Erickson,K. and Futcher,A.B.
The WHI1+ gene of Saccharomyces cerevisiae tethers cell division
cell size and is a cyclin homolog
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J. Mol. Biol. 225 (1), 53-65 (1992)
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Myol. Ccll. Biol. 12 (9), 3843-3856 (1992)
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Wol. Cell. Biol. 13 (12), 7901-7912 (1993)
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The yeast pyruvate kinase gene does not contain a string
non-preferred codons: revised nucleotide sequence
FEBS Lett. 247 (2), 312-316 (1989)
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S.Cerevislae YCT28p homolog; FLO9; GDH3; two alcohol/sorbitol dehydrogenase homologs; SIM1; CNE1. ACS1: S.pombe SPAC IF7.03 homolog; S.cerevislae Pip2p-138e transcription factor homolog; GCV3, glycine cleavage H protein; PTA1; FUN9 transcript, essential pene. S.pombe SPAC 24B1.08c homolog; CDC24; CLM3/MH1/DAF2; CYC3: PYK1; S.cerevislae ORF 0688 homolog; Renopus laevis GTP-binding protein DRG homolog; FUN12 transcript, essential gene: FUN19 transcript, cerevislae ORF 06105 homolog; FUN5 transcript, essential gene; FUN19 essential gene; FUN2 transcript, essential gene; FUN2 (AMP 2007) ENC2; CMS (AMP 2007) EN
                                                                                                                                                                                                                                                            Dumont, M.E., Ernst, J.F., Hampsey, D.M. and Sherman, F. Identification and sequence of the gene encoding cytochrome c heme. Iyase in the yeast Saccharomyces cerevisiae EMBO J. 6 (1), 235-241 (1987)
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Nucleotide sequence of the CLS4 (CDC24) gene of Saccharomyces
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Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6007-6011 (1988)
88320371
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Host function of MAK16: Gl arrest by a mak16 mutant of
                                                                                                          Ouery Match 98.6%; Score 224.8; DB 8; Length Best Local Similarity 99.1%; Pred. No. 6.6e-52; Matches 226; Conservative 0; Mismatches 2; Indels
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Usellette, B.F., Barton, A.B., Kaback, D.B. and Bussey, H.
LTE1 of Saccharomyces cerevisiae is a 1435 codon open reading frame that has sequence similarities to guanine nucleotide releasing
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Docteur Penfield Avenue, Montreal, Guebec, H3A 1B1, Canada
Sequence update which affects many coding regions
22 (bases 1 to 103682)
Jia.Y. and Cherry, J.M.
Direct Submission
Submitted (27.c2r-1997) Department of Genetics, Stanford
University, Saccharomyces Genome Database, Stanford, CA 94305-5126,
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Hall,J., Oucllettc,B.F.F., Keng,T., Barton,A.B., Su,Y., Davies,C.K.
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20 (bases I to 103682)
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Sutrave, P., Shafer, B., Strathern, J. and Hughes, S.
Isolation, identification and characterisation of the FUNI2 gene
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/note="tAL067C; Suppressor of sulfoxyde ethionine
resistance; similar to S. cerevisiae Yor28p Swiss-Prot
Accession Number P25621, with homology to allantoate
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The nucleotide sequence of chromosome I from Saccharomyces
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complement(4645, .6426)
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/organism-"Saccharomyces ccrevisiae"
/mol_type-"genomic DNA"
/strain="8288C/Ab972"
/db_xref-"taxon:4932"
/chromosome="1"
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URL: http://genome.www.stanford.edu/
e-mail: yeast-curator@genome.stanford.edu
Location/Qualifiers
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Unpublished (1992)
19 (bases 1 to 103682)
Volckaert,G. and Valle,G.
Unpublished (1997)
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15 (bases 99096 to 103271)
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61 GACGATTIGAAAGICTGTAAAAAATCCATITAIGACTTIAITGGGCIGCAAGAAACAC 120
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/product="Seolp: putative membrane protein"
/protein_id="AAC04968.1"
/db_xref="G1:595520"
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                                                                                                            Score 224.8; DB 8;
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             /citation=[8]
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